



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/030,225

DATE: 08/06/2002
TIME: 12:46:36

Input Set : A:\84335153.app
Output Set: N:\CRF3\08062002\J030225.raw

ENTERED

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3 <110> APPLICANT: OTA, TOSHIO
4     ISOGAI, TAKAO
5     NISHIKAWA, TETSUO
6     HIO, YURI
7     KENJI, YOSHIDA
8     MASUHO, YASUHIKO
10 <120> TITLE OF INVENTION: GROWTH AND DIFFERENTIATION FACTOR
12 <130> FILE REFERENCE: 084335/0153
14 <140> CURRENT APPLICATION NUMBER: 10/030,225
15 <141> CURRENT FILING DATE: 2002-01-08
17 <150> PRIOR APPLICATION NUMBER: JP 11/194179
18 <151> PRIOR FILING DATE: 1999-07-08
20 <150> PRIOR APPLICATION NUMBER: 60/159,586
21 <151> PRIOR FILING DATE: 1999-10-18
23 <160> NUMBER OF SEQ ID NOS: 14
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2981
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (58)..(1770)
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38 atg cgt gcg ctc cgc gac cga gcc ggg ctc ctc ctc tgc gtg ctg ctg      105
39 Met Arg Ala Leu Arg Asp Arg Ala Gly Leu Leu Leu Lys Val Leu Leu
40      1          5          10          15
41 ctg gcg gcg ctg ctg gag gcg gcg cta ggg ctc ccc gtg aag aag ccg      153
42 Leu Ala Ala Leu Leu Glu Ala Ala Leu Gly Leu Pro Val Lys Lys Pro
43      20          25          30
44 cgg ctc cgc gga cca cgg cct ggg agc ctc acg agg ctc gca gag gtc      201
45 Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val
46      35          40          45
47 tca gcc tcc cca gat cct agg cct ctg aag gaa gag gag gag gca cca      249
48 Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro
49      50          55          60
50 ctg ctc ccc aga acc cac ctg cag gca gag cca cac caa cat gga tgc      297
51 Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys
52      65          70          75          80
53 tgg act gtc act gag cca gca gcc atg acc cca ggc aac acc acc cct      345
54 Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro
55      85          90          95

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63	ccc agg acc cca gag gtt act ccg ttg cgg ctg gag ctg cag aag ctg	393
64	Pro Arg Thr Pro Glu Val Thr Pro Leu Arg Leu Glu Leu Gln Lys Leu	
65	100 105 110	
67	ccg gga ttg gcc agc aca acc ttg agt acc cct aac cct gat acc cag	441
68	Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln	
69	115 120 125	
71	gct tca gcc tcc cca gat cct agg cct ctg agg gaa gag gag gag gca	489
72	Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala	
73	130 135 140	
75	cga ctg ctc ccc aga acc cac ctg cag gca gag cta cac caa cat gga	537
76	Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gly	
77	145 150 155 160	
79	tgt tgg act gtc act gag cca gca gcc ctg acc cca ggg aat gcc acg	585
80	Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr	
81	165 170 175	
83	cct ccc agg acc cag gag gtt act ccc ttg ctg ctg gag ctg cag aag	633
84	Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys	
85	180 185 190	
87	ctg cca gaa ttg gtc cac gca acc ttg agt acc cct aac cct gat aac	681
88	Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn	
89	195 200 205	
91	cag gtg acc atc aag gtg gtg gag gac ccc cag gcc gag gtg tcg ata	729
92	Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile	
93	210 215 220	
95	gac ctg ttg gct gag ccc agc aat ccc ccg ccc cag gat acc ctt agc	777
96	Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser	
97	225 230 235 240	
99	tgg ctg ccc gcc ctc tgg ccc ttc ctc tgg gga gac tac aaa gga gag	825
100	Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu	
101	245 250 255	
103	gaa aaa gac agg gcc cca ggg gag aag ggg gag gaa aag gag gaa gac	873
104	Glu Lys Asp Arg Ala Pro Gly Glu Lys Gly Glu Glu Lys Glu Glu Asp	
105	260 265 270	
107	gag gac tat cct tca gag gat atc gag ggt gag gat caa gag gac aaa	921
108	Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys	
109	275 280 285	
111	gag gaa gat gag gaa gag cag gcg ctc tgg ttc aat gga act aca gac	969
112	Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp	
113	290 295 300	
115	aac tgg gac cag gcc tgg ctg gcc ccc ggg gat tgg gtc ttc aag gat	1017
116	Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp	
117	305 310 315 320	
119	tct gtc agc tac gac tat gag cct cag aag gag tgg agt ccc tgg tct	1065
120	Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser	
121	325 330 335	
123	ccc tgc agt ggg aac tgc agc act gcc aag cag cag agg act cgg ccc	1113
124	Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro	
125	340 345 350	
127	tgt ggc tat gcc tgc act gcc acc gag acc cgt acc tgt gac ctg ccc	1161

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128 Cys Gly Tyr Gly Cys Thr Ala Thr Glu Thr Arg Thr Cys Asp Leu Pro
129          355          360          365
131 tcc tgt cct ggc act gag gac aag gac acc ttg ggc ctc ccc agt gag 1209
132 Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu
133          370          375          380
135 gag tgg aag ctc ctg gcc cgc aat gct acg gac atg cat gat caa gat 1257
136 Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp
137 385          390          395          400
139 gtg gac agc tgt gag aag tgg ctg aac tgc aag agc gac ttc cta atc 1305
140 Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile
141          405          410          415
143 aag tat ctg agc cag atg ctg cgg gac ctg ccc agc tgc ccg tgt gcc 1353
144 Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala
145          420          425          430
147 tac cca ctg gag gcc atg gac agc cct gtg agc cta cag gac gag cac 1401
148 Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His
149          435          440          445
151 cag ggc cgc agc ttc cgg tgg agg gat gcc agt ggc cct cgc gag cgc 1449
152 Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg
153          450          455          460
155 ctg gac atc tac cag ccc acg gcg cgc ttc tgc ctg cgt tcc atg ctg 1497
156 Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu
157 465          470          475          480
159 tct ggg gag agc agc aca ctg gcc gcc cag cac tgc tgc tat gac gag 1545
160 Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu
161          485          490          495
163 gac agc cgg ctg ctg acc cgt ggc aag ggc gcc ggc atg ccc aac ctc 1593
164 Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu
165          500          505          510
167 atc agc acc gac ttc tca cct aag ctg cac ttc aag ttc gac acg acg 1641
168 Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr
169          515          520          525
171 ccc tgg atc ctg tgc aag ggg gac tgg agc cgc ctc cac gct gtg ctc 1689
172 Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu
173          530          535          540
175 cct ccc aac aac ggc cga gcc tgc acc gac aac ccc ctg gag gag gag 1737
176 Pro Pro Asn Asn Gly Arg Ala Cys Thr Asp Asn Pro Leu Glu Glu Glu
177 545          550          555          560
179 tac cta gca cag ttg cag gag gcc aag gag tac tagtgacggg gttgctgaac 1790
180 Tyr Leu Ala Gln Leu Gln Glu Ala Lys Glu Tyr
181          565          570
183 agacactgca gggagagggc agggggctgc tgctgttgca cgggagaact ttctggtag 1850
185 ggcctcacc cgcctctgcc cagacagggt gaggaaggg ctcctccagt gaggttggtc 1910
187 cgaggtctg tgccctctgc cagcagcccc gaagcagata tctcagtggg gttagtgaga 1970
189 aggttgaagg gtatgtaggg ccaggggtgg gtgtccctgg gagccctgga aatgtgcata 2030
191 tgtgcatgtg tctgcggggg cctccctctg ctgctctctg ggaccctggc cactcatttt 2090
193 tctcctcctt gggagctggg ctcttctgcc ctggctctgc acataagtgt tagccagcag 2150
195 ctcagaaaa atcccgatc ccgggatctg ccacagatca ctctactcc accctgatgg 2210
197 ccagcagagg aagggccact cttctcatgg gcacagccat cctttgccgg gggggcatcc 2270

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201 cctgccacga gccactgcac aggaggtat ctgtagcccc aagctgcctt tctgttgga 2390
203 accaacttta gtcttgggct gcaagccagc ccagctgagg cgaagtggac tccaggcagg 2450
205 gaatgggttg cccaattctg gtccctttcc ttgtctcagc cccctctgtt ctgctgattg 2510
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209 cagtagccag gcttgggtgg gttcagcact agctcgggac ggtgtgtcac acgtctatag 2630
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213 ggtgtaaatt ctcccagcag tgtcccatgt catgctgcca gcatcactga atgcactgaa 2750
215 ctccagattg ggaagagatg cacataatcg ctctcccggc acacctcatg cctcttccct 2810
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219 caactgtctc tgttcacaag agccacaaaa agttagggga ctccagtcct agccccaga 2930
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225 <211> LENGTH: 571
226 <212> TYPE: PRT
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234 20 25 30
236 Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val
237 35 40 45
239 Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro
240 50 55 60
242 Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys
243 65 70 75 80
245 Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro
246 85 90 95
248 Pro Arg Thr Pro Glu Val Thr Pro Leu Arg Leu Glu Leu Gln Lys Leu
249 100 105 110
251 Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln
252 115 120 125
254 Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala
255 130 135 140
257 Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gl
258 145 150 155 160
260 Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr
261 165 170 175
263 Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys
264 180 185 190
266 Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn
267 195 200 205
269 Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile
270 210 215 220
272 Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser
273 225 230 235 240
275 Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu
276 245 250 255

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278 Glu Lys Asp Arg Ala Pro Gly Glu Lys Gly Glu Glu Lys Glu Glu Asp
279                260                265                270
281 Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys
282                275                280                285
284 Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp
285                290                295                300
287 Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp
288 305                310                315                320
290 Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser
291                325                330                335
293 Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro
294                340                345                350
296 Cys Gly Tyr Gly Cys Thr Ala Thr Glu Thr Arg Thr Cys Asp Leu Pro
297                355                360                365
299 Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu
300                370                375                380
302 Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp
303 385                390                395                400
305 Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile
306                405                410                415
308 Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala
309                420                425                430
311 Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His
312                435                440                445
314 Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg
315                450                455                460
317 Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu
318 465                470                475                480
320 Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu
321                485                490                495
323 Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu
324                500                505                510
326 Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr
327                515                520                525
329 Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu
330                530                535                540
332 Pro Pro Asn Asn Gly Arg Ala Cys Thr Asp Asn Pro Leu Glu Glu Glu
333 545                550                555                560
335 Tyr Leu Ala Gln Leu Gln Glu Ala Lys Glu Tyr
336                565                570

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339 <210> SEQ ID NO: 3

340 <211> LENGTH: 30

341 <212> TYPE: RNA

342 <213> ORGANISM: Artificial Sequence

344 <220> FEATURE:

345 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially

346 Synthesized Oligo-cap Linker

348 <400> SEQUENCE: 3

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30

VERIFICATION SUMMARY

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